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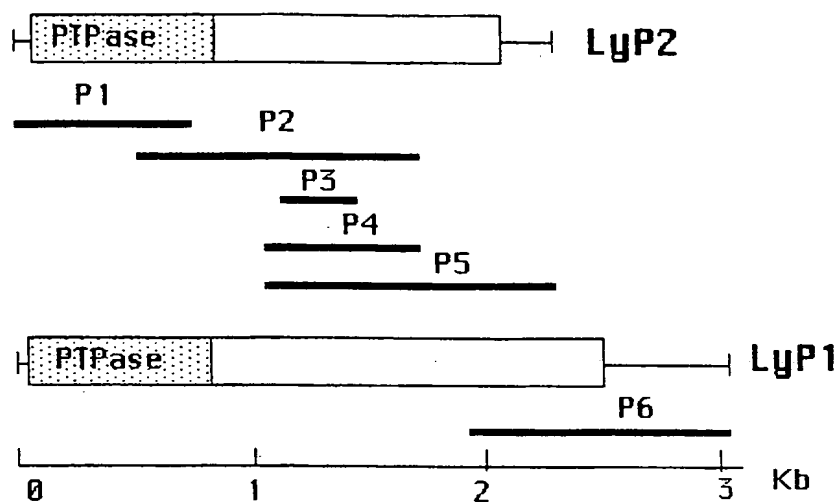


FIGURE 1

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| | | | | | | |
|-----------|------------|------------|-------------|-------------|-------------|-----|
| LyP1/2 | MDQREILQKF | LDEAQSCKIT | KEEFANEFLK | LKRQSTKYKA | DKTYPTTVAE | 50 |
| PEP | MDQREILQOL | LKEAQKCKLN | SEEFASEFLK | LKRQSTKYKA | DKIYPTTVAQ | 50 |
| Consensus | MDQREILQ.. | L.EAQ.KK.. | .EEFA.ZFLK | LKRQSTKYKA | DK.YPTTVA. | 50 |
| LyP1/2 | NAKNIKKNRY | KDILPYDYSR | VELSLITSDE | DSSYINANFI | KGVYGPKAYI | 100 |
| PEP | RPKNIKKNRY | KDILPYDHSL | VELSLITSDE | DSSYINASFI | KGVYGPKAYI | 100 |
| Consensus | ..KNIKKNRY | KDILPYD.S. | VELSL.TSDE | DSSYINA.FI | KGVYGPKAYI | 100 |
| LyP1/2 | ATQGPLSTTL | LDFWRMIWEY | SVLIIVMACM | EYEMGKKKCE | RYWAEPEGEMQ | 150 |
| PEP | ATQGPLSTTL | LDFWRMIWEY | RILVIIVMACM | EFEMGKKKCE | RYWAEPEGEMQ | 150 |
| Consensus | ATQGPLSTTL | LDFWRMIWEY | ..L.IVMACH | E.EMGKKKCE | RYWAEPEGE.Q | 150 |
| LyP1/2 | LEFGPFSVSC | EAEKRKSDYI | IRTLKVKFNS | ETRITYQFHY | KNWPDHVDPS | 200 |
| PEP | LQFGPFSISC | EAEKKKSDYK | IRTLKAKFNN | ETRITYQFHY | KNWPDHVDPS | 200 |
| Consensus | L.FGPFS.SC | EAEK.KSDY. | IRTLK.KFN. | ETR.IYQFHY | KNWPDHVDPS | 200 |
| LyP1/2 | SIDPILELIW | DVRCYQEDDS | VPICIHCSAG | CGRTGVICAI | VDYTWMLLKD | 250 |
| PEP | SIDPILQLIW | DMRCYQEDDC | VPICIHCSAG | CGRTGVICAV | -DYTWMLLKD | 249 |
| Consensus | SIDPIL.LIW | D.RCYQEDD. | VPICIHCSAG | CGRTGVICA. | .DYTWMLLKD | 250 |
| LyP1/2 | GIIPENFSVF | SLIREMRTOR | PSLVQTQEQY | ELVYNAVLEL | FKROMDVIRD | 300 |
| PEP | GIIPKNFSVF | NLIQEMRTOR | PSLVQTQEQY | ELVYSAVLEL | FKRHMDVISD | 299 |
| Consensus | GIIP.NFSVF | .LI.EMRTOR | PSLVQTQEQY | ELVY.AVLEL | FKR.MDVI.D | 300 |
| LyP1/2 | KHSGTESQAK | HCIPKKNHTL | QADSYSPNLP | KSTTKAAKMM | NQOR---TKM | 347 |
| PEP | NHLGREIQAQ | CSIPEQSLTV | EADSCPLDLP | KNAMRDVKT | NQHSKOGAEA | 349 |
| Consensus | .H.G.E.QA. | ..IPE...T. | .ADS....LP | K.....K.. | NQ..... | 350 |
| LyP1/2 | EIKESSSFDF | RTSEISAKKE | LVLHPAKSST | SFDFLELNYS | FDKNADTTMK | 397 |
| PEP | ESTGGSSLGL | RTSTMNAEEE | LVLHSAKSSP | SFNCLELNCG | CNNKAVITRN | 399 |
| Consensus | E....SS... | RTS...A.EE | LVLH.AKSS. | SF...LELN.. |A..T.. | 400 |

FIGURE 2

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| | | | | | | | |
|-----------|------------|------------|------------|------------|--------------|------------|-----|
| LyP1/2 | WQTKAFFIVG | EPLQKHOSLD | LGSLLFEGCS | NSKPVNAAGR | YFNSKVPITR | 447 | |
| PEP | GQARASPVVG | EPLQKYQSLD | FGSMLFGSCP | SALPINTADR | YHNSKGPVKR | 449 | |
| Consensus | .Q..A.P.VG | EPLQK.QSLD | .GS.LF..C. | ...P.N.A.R | Y.NSK.P..R | 450 | |
| LyP1/2 | TKSTPFELIQ | QRETKEVDSK | ENFSYLESQP | HDS-CFVEMQ | AQKVMHVSSA | 496 | |
| PEP | TKSTPFELIQ | QRKTNDLAVG | DGFSCLESQ | HEHYSLELO | VORVAHVSS | 499 | |
| Consensus | TKSTPFELIQ | QR.T..... | ..FS.LESQ. | H.....E.Q | .Q.V.HVSS. | 500 | |
| LyP1/2 | ELNYSLPYDS | KHQIRNASNV | KHHDSSALGV | YSYIPLVENP | YFSSWPPSGT | 546 | |
| PEP | ELNYSLPGAC | -----DASCV | PRHSPGALRV | HLTSLAEDP | YFSSSPNSA | 544 | |
| Consensus | ELNYSLP... |AS.V | ..H...AL.V | ..Y..L.E.P | YFSS.PP... | 550 | |
| LyP1/2 | SSKMSLDLPE | KODGTVPFSS | LLPTSSTSLF | SYNSHNSLS | LNSPTNISSL | 596 | |
| PEP | DSKMSFDLPE | KODGATSPGA | LLPASSTTSF | FYSNPHDSL | MNTLTFSPP | 594 | |
| Consensus | .SKMS.DLPE | KODG...P.. | LLP.SST..F | .Y.N.H.SL. | .N...T...S.. | 600 | |
| LyP1/2 | LNQESAVLAT | APRIDDEIPP | ***** | PLPVRTPESE | IVVEEAGEFS | PNVPSKLSA | 646 |
| PEP | LNQETAVEAP | SRRTDDEIPP | ***** | PLPERTPESE | IVVEEAGEPS | PRVTESE--P | 642 |
| Consensus | LNQE.AV.A. | ..R.DDEIPP | PLP.RTPESF | IVVEEAGE.S | P.V...SL... | 650 | |
| LyP1/2 | VKVKIGTSLE | WGGTSEPKKF | DDSVILRPSK | SVKLRSPKSE | LHQDRSSPPP | 696 | |
| PEP | LVVTFGASPE | CSGTSEMKS- | HDSVGFTPSK | NVKLRSPKSD | RHQDGSP-PP | 690 | |
| Consensus | ..V..G.S.E | ..GTSE.K.. | .DSV...PSK | .VKLRSPKS. | .HQD.S...PP | 700 | |
| LyP1 | ***** | PLPERTLESF | FLADEDCMQA | QSIETYSTSY | PDTMENSTSS | KQTLKTPGKS | 746 |
| PEP | ***** | PLPERTLESF | FLADEDCIQA | QAVQTSSTSY | PETTENSTSS | KQTLRTPGKS | 740 |
| Consensus | ***** | PLPERTLESF | FLADEDC.QA | Q...T.STSY | P.T.ENSTSS | KQTL.TPGKS | 750 |
| LyP1 | FTRSKSLKIL | RNMKKSICNS | ***** | CPNKPESV | QSNSSSFLN | FGFANRFSKP | 796 |
| PEP | FTRSKSLKIF | RNMKKSVCNS | ***** | SSPSKPTERV | QPKNSSSFLN | FGFGNRFSKP | 790 |
| Consensus | FTRSKSLKI. | RNMKKS.CNS | ..P.KP.E.V | Q..NSSSFLN | FGF.NRFSKP | 800 | |
| LyP1 | ***** | KGPRNPPPTW | NI | | | 808 | |
| PEP | ***** | KGPRNPPSAW | NM | | | 802 | |
| Consensus | ***** | KGPRNPP..W | N. | | | | |

↓ LyP2
GKNFSWL 692

FIGURE 2 CONT'D

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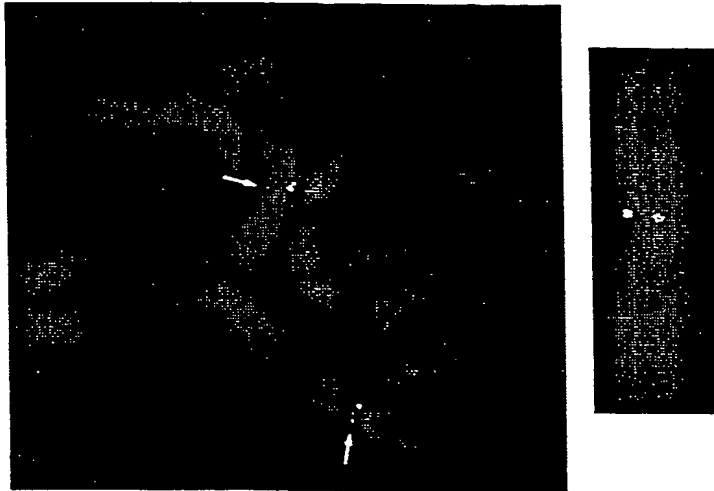


FIGURE 3A

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Chromosome 1

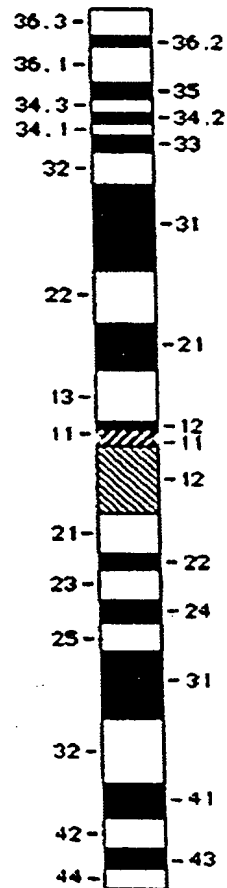


FIGURE 3B

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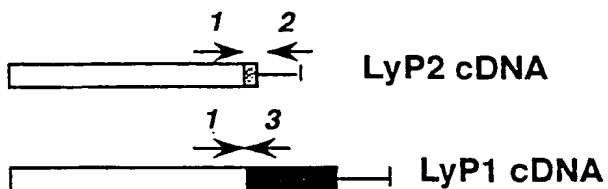
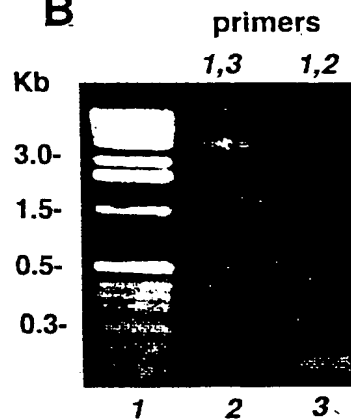
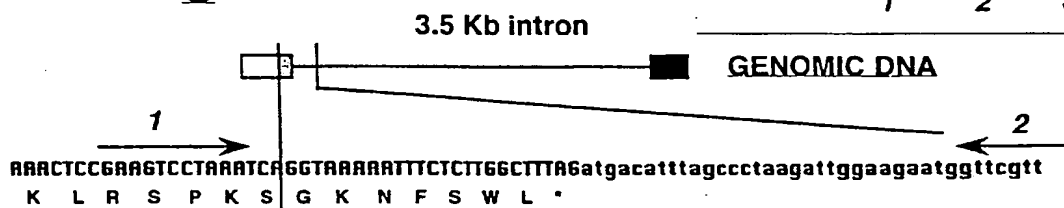
A**B****C**

FIGURE 4

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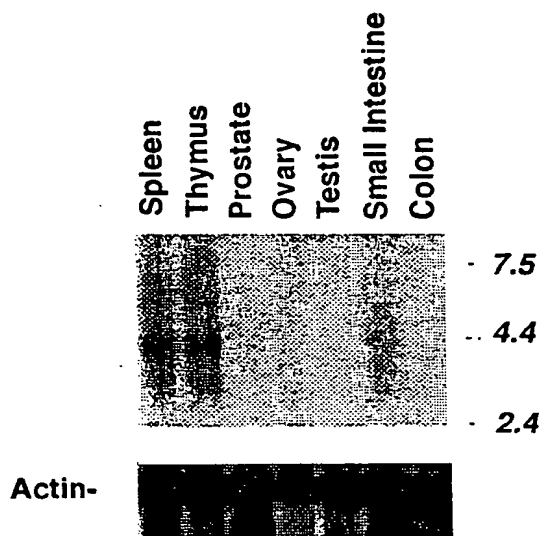


FIGURE 5A

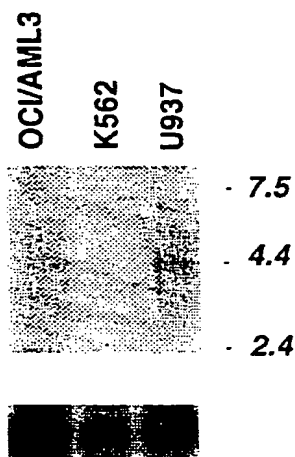


FIGURE 5B

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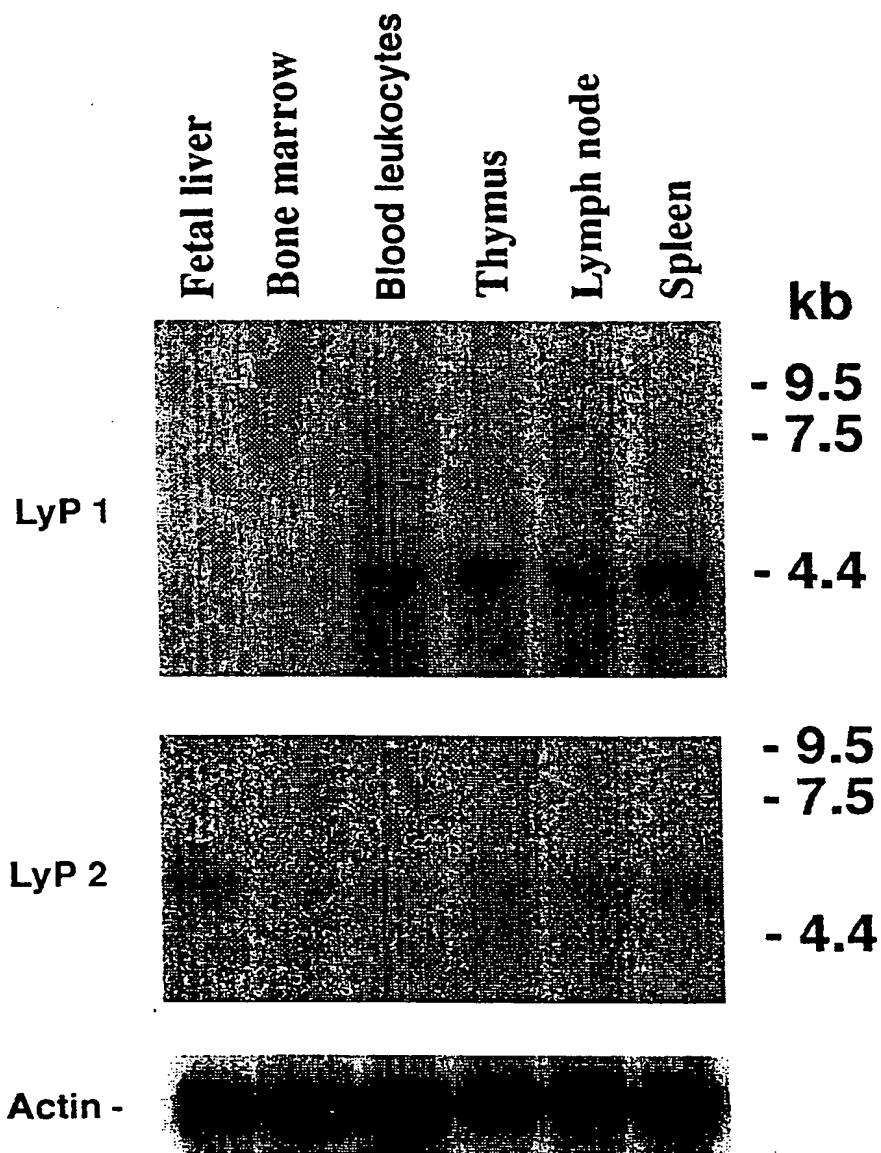


FIGURE 5C

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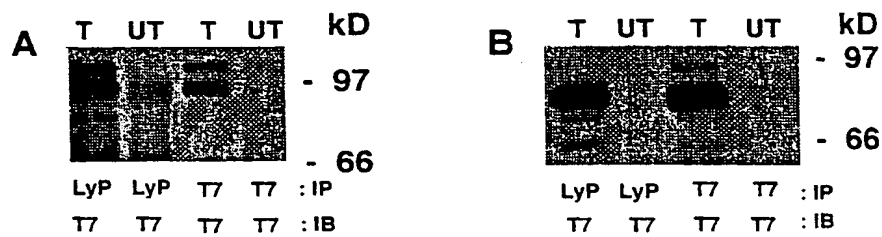


FIGURE 6

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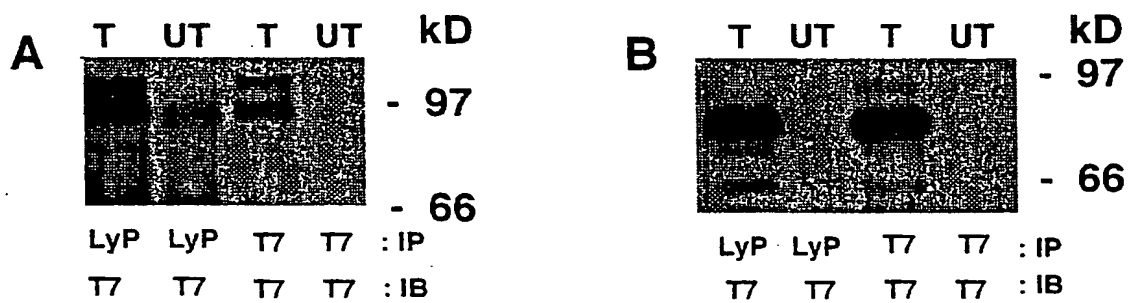


FIGURE 7

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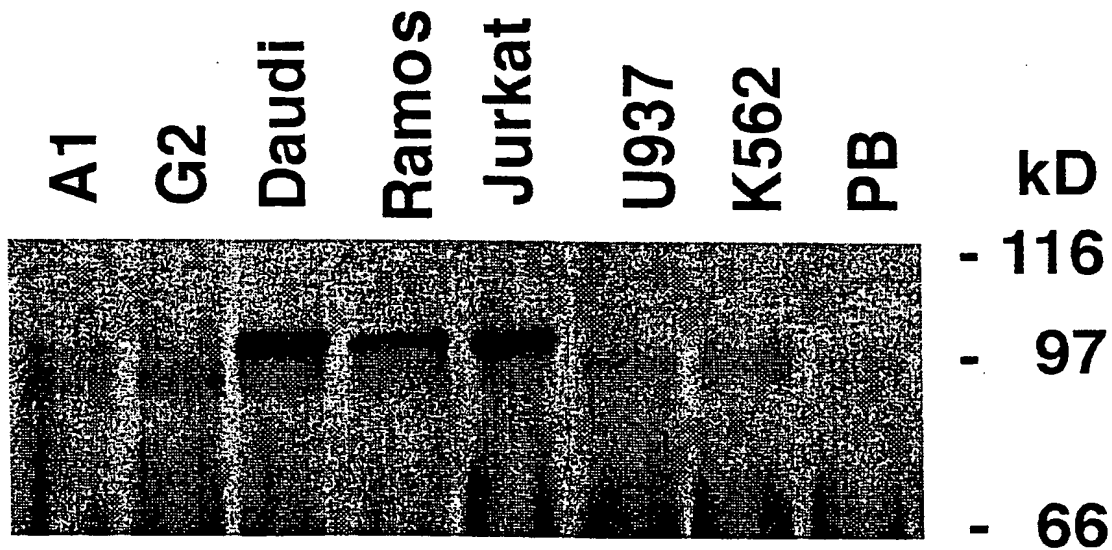


FIGURE 8

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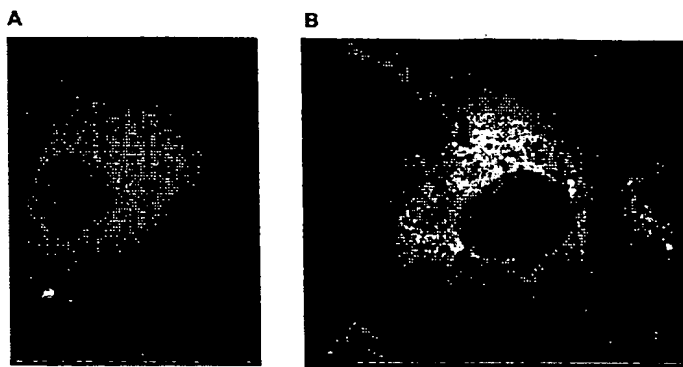


FIGURE 9

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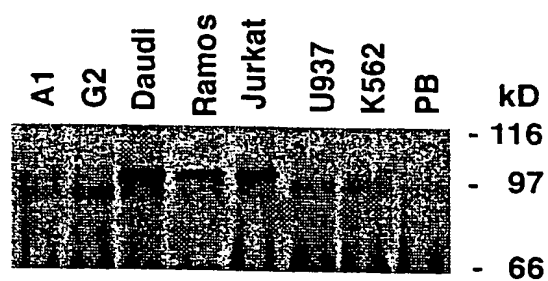


FIGURE 10

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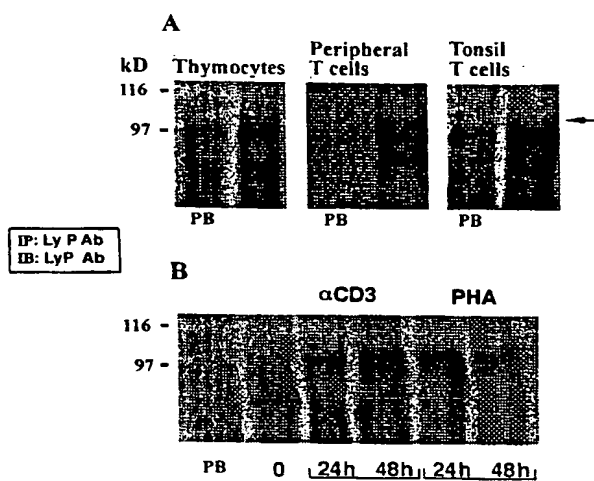


FIGURE 11

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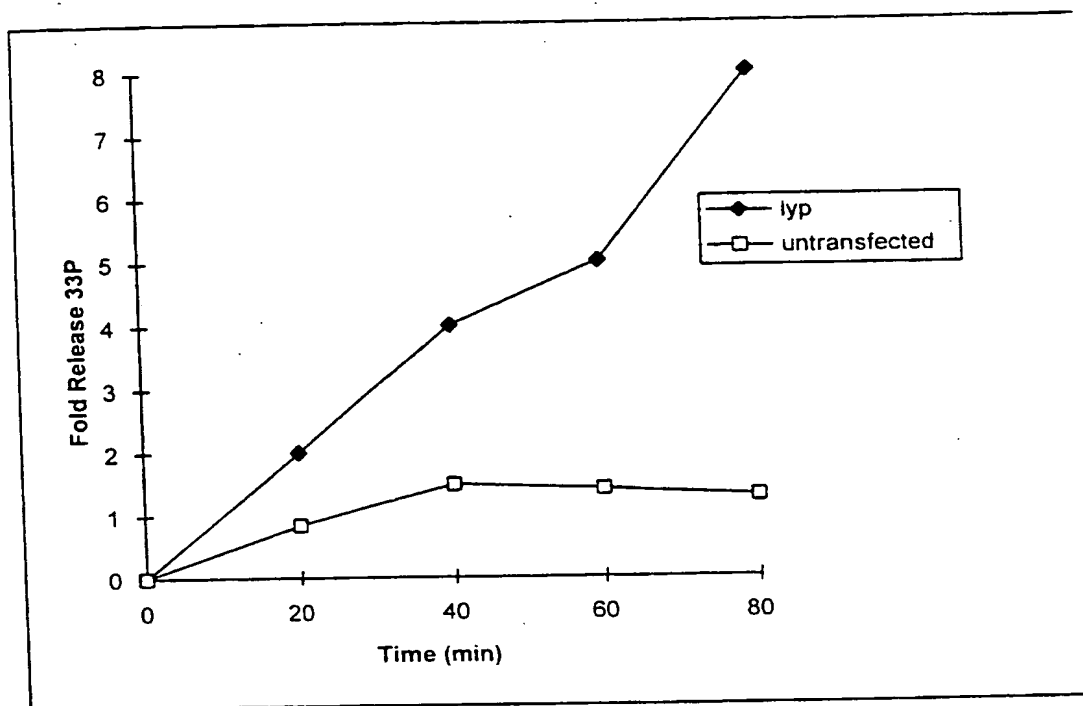


FIGURE 12

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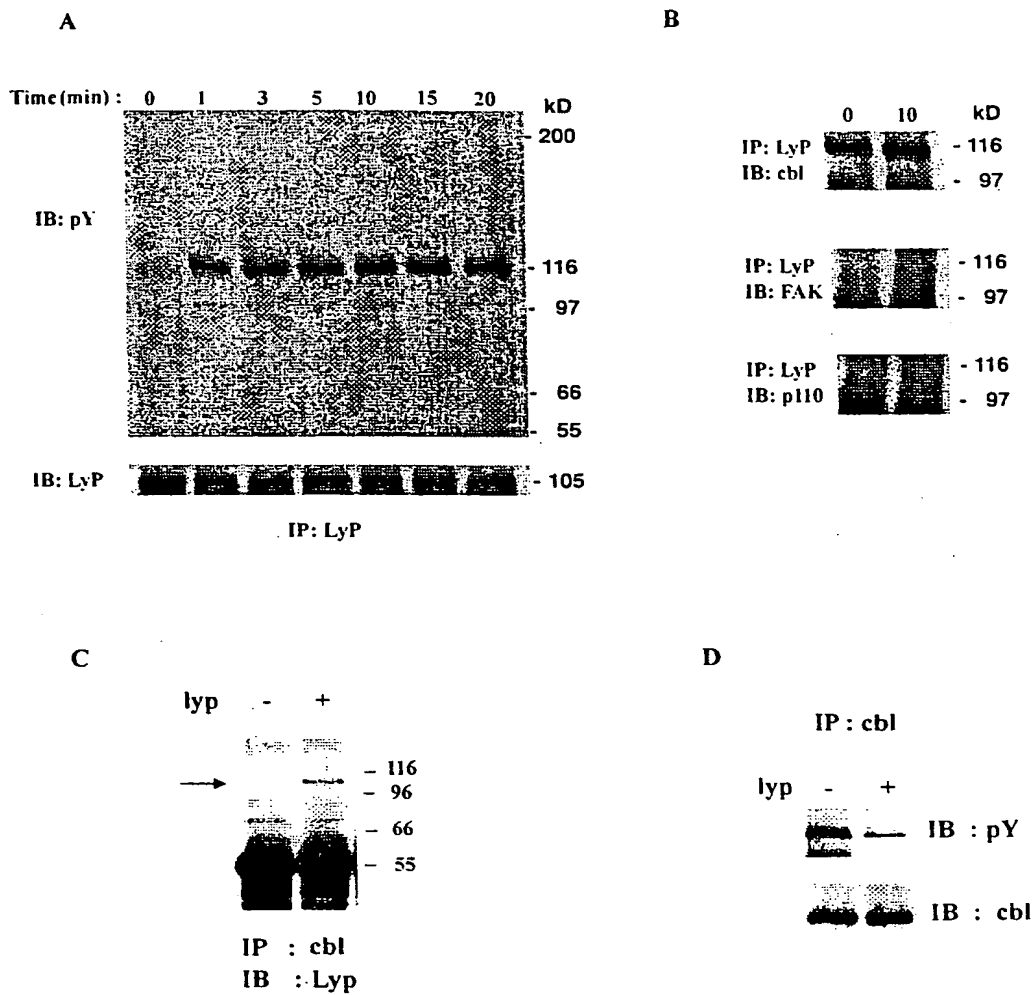


FIGURE 13

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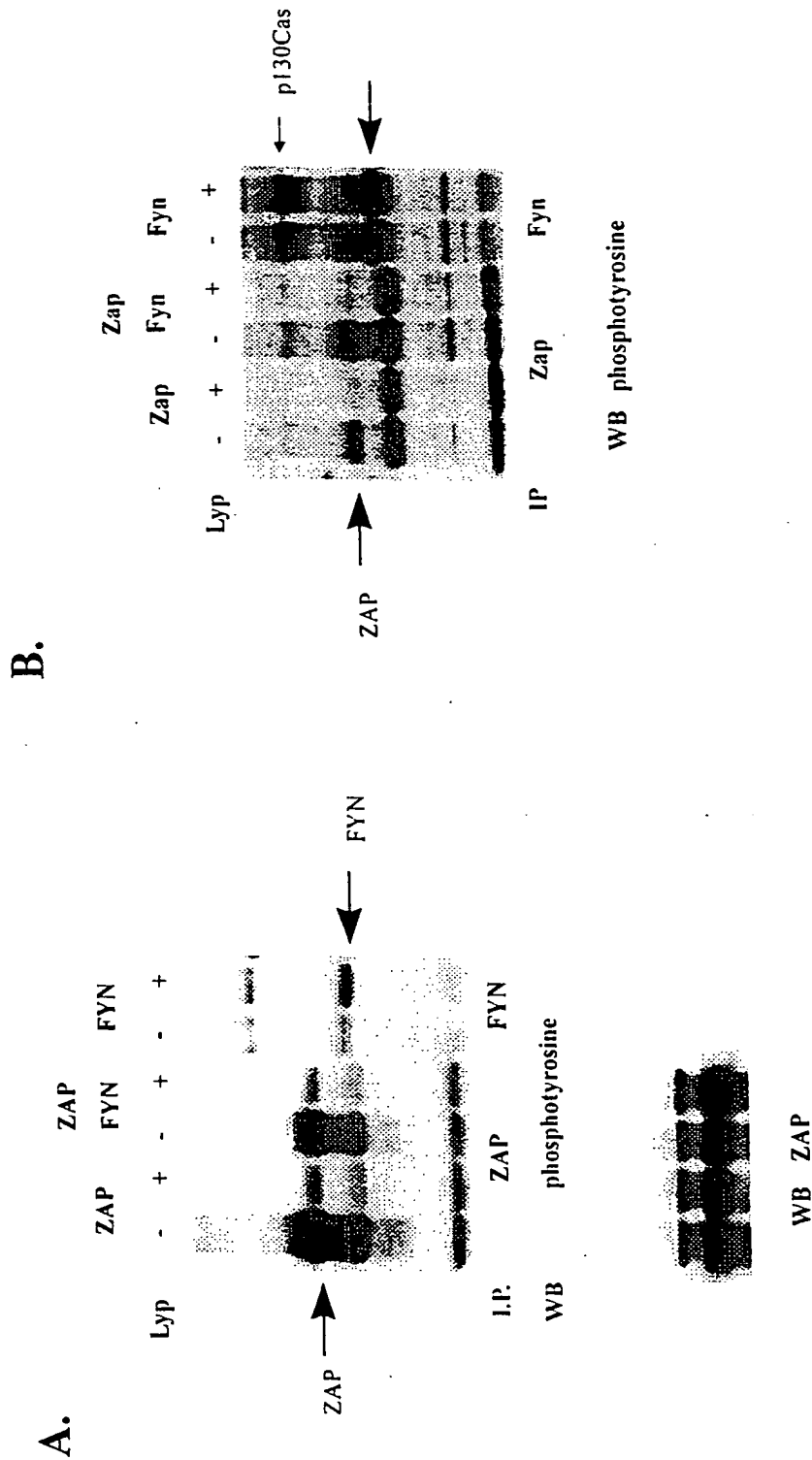
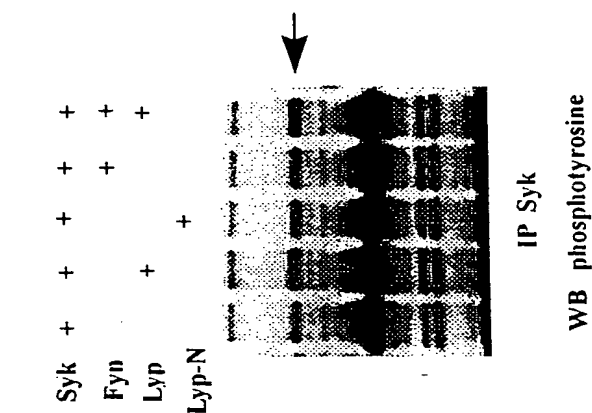


FIGURE 14

D.



C.

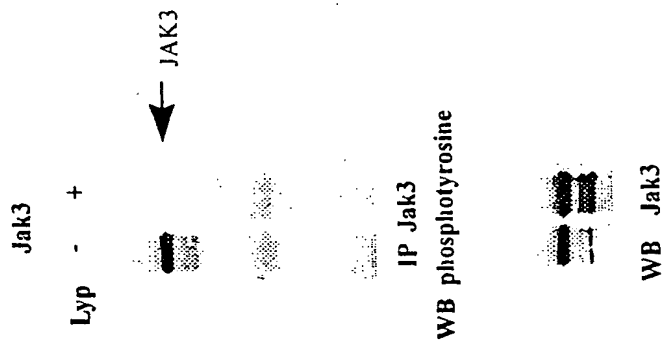


FIGURE 15